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# Dissertation Summary

There is scanty data on the nature and extent of co-infection with hepatitis B virus (HBV) and Human Immunodeficiency virus (HIV) in Zimbabwe. Co-infection with HBV and HIV is associated with HBV reactivation, HBV persistence, severe liver disease, liver fibrosis, cirrhosis, liver cancer and early death (Thio *et al.*, 2002; McMahon, 2009; Kew, 2012). The current study determined the prevalence of HBV-HIV coinfection among untreated HIV patients in Harare city. It also assessed whether patient demographics like age and sex, host immune status indicated by CD4+ T cell counts and liver fibrosis indicated by non-invasive markers FIB-4 and APRI, were associated with HBV-HIV co-infection. In addition, HBV and HIV genetic variants in the Harare cohort were sequenced and analyzed by phylogenetic analysis to identify genotypes and variants such as drug resistance mutations. Of the 176 pre-HIV treatment adults recruited, 19 (10.8%) were positive for hepatitis B surface antigen (HBsAg) i.e. were HBV-HIV co-infected, notably among male patients (p=0.009). Interestingly, lower CD4+ T cell counts (p=0.016) and higher fibrosis markers FIB-4 and APRI (p=0.0001) were associated with HBV-HIV co-infection in this cohort. Out of the 19 HBsAg-positive samples,12 had detectable HBV DNA and of these, 4 were successfully sequenced in the basal core promoter/precore (BCP/PC) and small surface antigen regions while 3, with high HBV viral load, in the whole HBV genome. All the 7 sequenced HBV isolates were classified as HBV subgenotype A1 by phylogenetic analysis. BCP/PC mutations like 1762T and 1764A, associated with liver cancer development, were identified. Mutations in the small surface antigen that are potentially associated with false positivity by some diagnostic assays i.e M133I/T and D144G were detected in 2 out of 7 isolates. Surprisingly, PreS2 deletion mutations were also identified in 2 out of the 3 full HBV sequences, one of which concurrently had a PreS1 deletion, all associated with intrahepatic HBsAg retention, ER stress and liver cancer. For HIV, 164 isolates were successfully sequenced in the *protease-reverse transcriptase* regions. All except one isolate (99.4%) were classified as HIV-1 subtype C. Interestingly, 9.8% (16/164) of these HIV isolates had drug resistance mutations associated with non-nucleoside reverse transcriptase inhibitors (NNRTIs) like the K103N, Y181C, predominantly among female patients suggesting undisclosed antiviral exposure or transmitted drug resistance. In conclusion, our data showed a high prevalence of HBV-HIV coinfection in our HIV cohort therefore rigorous HBV screening and treatment with dual active drugs e.g. Tenofovir-based regimens were recommended.

**References**

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